1: Nippon Rinsho 1996 Apr;54(4):986-991

Related Articles

[Detailed deletion map of chromosomal arm 9q in esophageal s cell carcinoma].

[Article in Japanese]

Miura K, Nakamura Y.

Laboratory of Molecular Medicine, University of Tokyo.

We examined loss of heterozygosity (LOH) in 37 esophageal squamous cel using microsatellite markers mapped to 9q31-34.1. Partial or interstitial del detected in 13 of them and the detailed deletion map defined a commonly d between the D9S262 and D9S154 loci at 9q31-q32. The genetic distance w to be approximately 4 cM. To narrowly define the commonly deleted regio six microsatellite markers from YAC (yeast artificial chromosome) clones deleted region. As the distal 9q region also has been implicated as the site o suppressor gene(s) related to squamous cell carcinomas of other tissues, ou provides useful information for attempts to identify a common gene for car this cell type.

Publication Types:
- Review
- Review, tutorial

PMID: 8920661 [PubMed - indexed for MEDLINE]

1: Mamm Genome 1995 Sep;6(9):586-591

Mouse H2 congenic intervals: analysis and use for mapping.

Jiang PP, Hansen TH, Shreffler DC, Miller RD.

Department of Genetics, Washington University School of Medicine, St. Lc 63110, USA.

In this study we exploit the unique genetic resource of inbred mouse major histocompatibility complex (H2) congenic and recombinant strains to const resolution map of microsatellite loci in and around the H2 region, as well as independent genetic map of other loci on mouse Chromosome (Chr) 17. Mi loci were analyzed in 11 C57BL/10 (B10) strains to determine the size of th interval in each. The length of the congenic interval found in each strain va Interestingly, the intervals were generally smaller than statistical expectatio the observed congenic intervals were still sufficiently long that these strains wild-derived H2 congenics are an important source of genetic variability. T ends of the various congenic intervals and the recombinants were used to cc map. This map will be useful for physical cloning and to help localize nove evidence of the mapping application of congenic strains, locational informa derived about Trp53-ps and Stl.

PMID: 8535063 [PubMed - indexed for MEDLINE]

1: Genomics 1995 Aug 10;28(3):566-569

Genetic association between chromosome 8 microsatellite (MS Werner syndrome (WRN): chromosome microdissection and homozygosity mapping.

Ye L, Nakura J, Mitsuda N, Fujioka Y, Kamino K, Ohta T, Jinno Y, N Miki T, Ogihara T.

Department of Geriatric Medicine, Osaka University Medical School, Japar

Werner syndrome (WRN) is an autosomal recessive disorder characterized aging that has been mapped to the short arm of chromosome 8, 8p11.2-p12. genetic map around the WRN region, we have isolated eight microsatellites region from a microdissection library. We typed members of Japanese fami WRN on the basis of homozygosity mapping analysis. There was no obliga recombination between the WRN locus and microsatellite clone, MS8-134 The maximum lod score was 20.28 at theta = 0.00. Alleles for MS8-134 sh association with WRN in a case-control study (OR = 3.55, 95% CI 1.56-8.0 Such microsatellites from a microdissection library of the definite chromos may be useful for positional cloning of the WRN gene.

PMID: 7490095 [PubMed - indexed for MEDLINE]

1: Genomics 1996 Mar 15;32(3):458-461 Related Articles

IDEAL

Physical mapping of 49 microsatellite markers on chromosome correlation with the genetic linkage map.

Reguigne-Arnould I, Faure S, Chery M, Mota-Viera L, Mollicone R, C Oriol R, Couillin P.

INSERM U178, Villejuif, France. arnould@infobiogen.fr

We have regionally localized 49 microsatellite markers developed by Genet panel of previously characterized somatic cell hybrids that retain fragments chromosome 19. The tight correlation observed between the physical and th orders of the microsatellites provide cytogenetic anchorages to the genetic r propose a position for the centromere just above D19S415, from the study c hybrids, each of which retains one of the two derivatives of a balanced trans (1;19)(q11;q11). Microsatellites, which can be identified by a standard PCR useful tools for the localization of disease genes and for the establishment o cosmid contigs. These markers can also judiciously be used for the characte new hybrid cell line panels. We report such a characterization of 11 clones, were obtained by irradiation-fusion. Using the whole hybrid panel, we were define the order of 12 pairs of genetically colocalized microsatellites. As ex gene mapping by the combined use of microsatellites and hybrid cell lines, assigned the PVS locus between the 19q13.2 markers D19S417 and D19S4 confirmed the locations of fucosyltransferase loci FUT1, FUT2, and FUT5.

PMID: 8838811 [PubMed - indexed for MEDLINE]

1: Chromosome Res 1999;7(8):635-640

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Differentiation of Z and W chromosomes revealed by replicati and FISH mapping of sex-chromosome-linked DNA markers i cassowary (Aves, Ratitae).

Nishida-Umehara C, Fujiwara A, Ogawa A, Mizuno S, Abe S, Yoshida

Chromosome Research Unit, Faculty of Science, Hokkaido University, Sap

We identified sex chromosomes of the double-wattled cassowary (Casuariu by a replication banding method. The acrocentric Z chromosome, the fifth l males and slightly smaller W chromosome show no sign of heterochromati share a nearly identical banding pattern in the distal half of the long arm. Tl chromosomes were further characterized by FISH with three probes linked W chromosome in most avian species examined thus far. Contrary to the sit chicken, we obtained positive signals with Z-specific ZOV3 and W-specific the distal region of both Z and W chromosomes. However, IREBP signals l the proximal half of the Z chromosome were not detected on the W chromo structural rearrangements such as deletions and inversions might have been step of W chromosome differentiation from an ancestral homomorphic pair species.

PMID: 10628664 [PubMed - indexed for MEDLINE]

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A comprehensive microsatellite linkage map of the chicken gen

Groenen MA, Crooijmans RP, Veenendaal A, Cheng HH, Siwek M, va JJ.

Department of Animal Breeding, Wageningen Institute of Animal Sciences, Agricultural University, The Netherlands. martien.groenen@alg.vf.wau.nl

A comprehensive linkage map of the chicken genome has been developed b analysis of 430 microsatellite markers within a cross between two extreme l The population used to construct the linkage map consists of 10 families wi 458 F2 individuals. The number of informative meioses per marker varied f 900 with an average of 400. The markers were placed into 27 autosomal lin and a Z-chromosome-specific linkage group. In addition, 6 markers were ur which was Z chromosome specific. The coverage within linkage groups is : Although, as in other species, the genetic map of the heterogametic sex (fen shorter than the genetic map of the homogametic sex (male), the overall dif length is small (1.15%). Forty-five of the markers represent identified genes Database homology searches with the anonymous markers resulted in the id of a further 9 genes, bringing the total number of genes/ESTs on the current The mapping of these genes led to the identification of two new regions of synteny between human and chicken and confirmed other previously identif of conserved synteny between human and chicken. The linkage map has 21 common with the linkage maps based on the East Lansing and Compton ref populations, and most of the corresponding linkage groups in the different r readily aligned.

PMID: 9598314 [PubMed - indexed for MEDLINE]